SEQUENCE LISTING

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KITAMURA, TOSHIO

<120> METHOD FOR SCREENING CANDIDATE COMPOUNDS FOR ANTITUMOR DRUG

<130> 084335/0129

<140>
<141>

<150> PCT/JP99/04450
<151> 1999-08-19

<150> JP 1998-233729
<151> 1998-08-20

<160> 10

<170> PatentIn Ver. 2.1

<210> 1
<211> 319
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(318)
<223> FLT3/ITD gene (Mt1); partial sequence

<400> 1

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caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc   48
Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
  1               5                  10                  15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa tat gat   96
Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
            20                  25                  30

ctc aaa tgg gag ttt cca aga gaa aat tgc tcc tca gat aat gag tac   144
Leu Lys Trp Glu Phe Pro Arg Glu Asn Cys Ser Ser Asp Asn Glu Tyr
        35                  40                  45

ttc tac gtt gat ttc aga gaa tat gaa tat gat ctc aaa tgg gag ttt   192
Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
    50                  55                  60

cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt   240
Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
65                  70                  75                  80
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gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc   288
Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
                 85                  90                  95

tca atc cag gtt gcc gtc aaa atg ctg aaa g                       319
Ser Ile Gln Val Ala Val Lys Met Leu Lys
            100                 105
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<210> 2
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<223> FLT3/ITD (Mt1); partial sequence
ITD region (42)..(68)

<400> 2

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Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
  1               5                  10                  15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
             20                  25                  30

Leu Lys Trp Glu Phe Pro Arg Glu Asn Cys Ser Ser Asp Asn Glu Tyr
         35                  40                  45

Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
     50                  55                  60

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
 65                  70                  75                  80

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
                 85                  90                  95

Ser Ile Gln Val Ala Val Lys Met Leu Lys
            100                 105
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<210> 3
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(297)
<223> FLT3/ITD gene (Mt2); partial sequence

<400> 3

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caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc   48
Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
  1               5                  10                  15
```

```
tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa tat gat    96
Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
             20                  25                  30

ctc aaa agc tcc tca gat aat gag tac ttc tac gtt gat ttc aga gaa   144
Leu Lys Ser Ser Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu
         35                  40                  45

tat gaa tat gat ctc aaa tgg gag ttt cca aga gaa aat tta gag ttt   192
Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe
     50                  55                  60

ggg aag gta cta gga tca ggt gct ttt gga aaa gtg atg aac gca aca   240
Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val Met Asn Ala Thr
 65                  70                  75                  80

gct tat gga att agc aaa aca gga gtc tca atc cag gtt gcc gtc aaa   288
Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys
                 85                  90                  95

atg ctg aaa g                                                    298
Met Leu Lys
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<210> 4
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<223> FLT3/ITD (Mt2); partial sequence
ITD region (35)..(54)

<400> 4

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Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
  1               5                  10                  15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
             20                  25                  30

Leu Lys Ser Ser Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu
         35                  40                  45

Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe
     50                  55                  60

Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val Met Asn Ala Thr
 65                  70                  75                  80

Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys
                 85                  90                  95

Met Leu Lys
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<210> 5
<211> 271

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(270)
<223> FLT3/ITD gene (Mt3); partial sequence

<400> 5
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Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
1 5 10 15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa atg gga 96
Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Met Gly
20 25 30

atg ggg gga gaa tgt aat ccc ggg aga caa gat ctc aaa tgg gag ttt 144
Met Gly Gly Glu Cys Asn Pro Gly Arg Gln Asp Leu Lys Trp Glu Phe
35 40 45

cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt 192
Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
50 55 60

gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc 240
Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
65 70 75 80

tca atc cag gtt gcc gtc aaa atg ctg aaa g 271
Ser Ile Gln Val Ala Val Lys Met Leu Lys
85 90

<210> 6
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<223> FLT3/ITD (Mt3); partial sequence
ITD region (31)..(42)

<400> 6
Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
1 5 10 15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Met Gly
20 25 30

Met Gly Gly Glu Cys Asn Pro Gly Arg Gln Asp Leu Lys Trp Glu Phe
35 40 45

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
50 55 60

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
65 70 75 80

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Ser Ile Gln Val Ala Val Lys Met Leu Lys
                85                  90


<210> 7
<211> 271
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(270)
<223> FLT3/ITD gene (Mt4); partial sequence

<400> 7
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Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
  1               5                  10                  15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gat gag tac   96
Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Asp Glu Tyr
             20                  25                  30

ttc tac gtt gat ttc aga gaa tat gaa tat gat ctc aaa tgg gag ttt   144
Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
         35                  40                  45

cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt   192
Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
     50                  55                  60

gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc   240
Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 65                  70                  75                  80

tca atc cag gtt gcc gtc aaa atg ctg aaa g                        271
Ser Ile Gln Val Ala Val Lys Met Leu Lys
                85                  90


<210> 8
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<223> FLT3/ITD (Mt4); partial sequence
      ITD region (30)..(40)

<400> 8
Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
  1               5                  10                  15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Asp Glu Tyr
             20                  25                  30
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Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
35 40 45

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
50 55 60

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
65 70 75 80

Ser Ile Gln Val Ala Val Lys Met Leu Lys
85 90

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: A primer for amplifying human FLT3/ITD genes

<400> 9
caacaattgg tgtttgtctc ctctt 25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: A primer for amplifying human FLT3/ITD genes.

<400> 10
catgatatct cgagccaatc caaag 25